This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2015.011aD***	(to be completed by ICTV officers)

Short title: One new species, *Erinnyis ello granulovirus*, **in the genus** ***Betabaculovirus***
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	**1** ☒	**2** ☒	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☐	**10** ☒

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List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	Baculoviridae/Nudiviridae Study Group

ICTV Study Group comments (if any) and response of the proposer:

ICTV has the following rule for distinguishing between names of virus isolates and names of species: Species names are entirely italicized, and names of virus isolates and genome sequences are entirely in regular type (e.g. no part is italicized). While historically baculovirologists have italicized the host genus and species in the names of virus isolates, this is no longer an accepted convention.

Response: We have followed the ICTV rules for the proposed species.

Proposal moved to the latest TP template.

Date first submitted to ICTV:	5/27/15
Date of this revision (if different to above):	9/23/15

ICTV-EC comments and response of the proposer:

9/23/15: The tree in Figure 1 was replaced with a comparable tree showing that the proposed species is different and distinct from the other two *Betabaculovirus* species discussed at EC47, *Agrotis segetum granulovirus* and *Spodoptera frugiperda granulovirus*.

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

Code	***2015.011aD***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Betabaculovirus***
Subfamily:	
Family:	***Baculoviridae***
Order:	

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Erinnyis ello granulovirus	Erinnyis ello granulovirus (ErelGV) isolate S86	KJ406702

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
    - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
    - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

The Erinnyis ello granulovirus (ErelGV) isolate S86 (Southern Brazil in 1986) of the proposed species can be identified as belonging to the genus *Betabaculovirus* on the basis of host species of the insect order Lepidoptera; circular double-stranded DNA genome of 102 kbp, gene content characteristic of other betabaculoviruses; relationships to other baculoviruses as inferred by molecular phylogeny; occlusion bodies with a characteristic size and shape; and rod-shaped virions consisting of nucleocapsids enveloped singly into the granule (Ardisson-Araujo et al., 2014). Figure 1 shows the relationships of the virus in the proposed species to viruses in other recognized species in the family *Baculoviridae*, as determined from the concatenated alignment of the nucleotide sequences of the currently defined 37 baculovirus core genes (Garavaglia et al., 2012). Reference isolate for the proposed species occurs in the *Betabaculovirus* clade in the Figure 1 phylogram.

Distinctions among species of the *Baculoviridae* have been based on DNA restriction endonuclease fragment patterns and comparisons of nucleotide and predicted amino acid sequences from various genes. A proposed species demarcation criterion was published in 2006 that is based on pairwise nucleotide distances estimated using the Kimura 2-parameter model of nucleotide substitution (Jehle et al., 2006). The pairwise distances of the viral sequences of ErelGV to other betabaculoviruses for both the single locus and the concatenated alignments are well in excess of 0.05 substitutions/site (Tables 1 and 2, red type). Branch length in the Figure 1 phylogram separating this virus from its closest relatives are in a range that is comparable to the branch lengths separating viruses in other recognized betabaculovirus species. Distinctive genome features and gene compositions for this virus are detailed in the publication describing the genome.

Finally, *Errinyis ello granulovirus* is different and distinct from the other two new *Betabaculovirus* species proposed in 2015, *Agrotis segetum granulovirus* and *Spodoptera frugiperda granulovirus*.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

***Baculoviridae* core genes and proposed species demarcation criteria**

Jehle, J. A., Lange, M., Wang, H., Hu, Z., Wang, Y., Hauschild, R. (2006). Molecular identification and phylogenetic analysis of baculoviruses from Lepidoptera. Virology 346, 180-93.

Garavaglia, M. J., Miele, S. A., Iserte, J. A., Belaich, M. N., Ghiringhelli, P. D. (2012). The ac53, ac78, ac101, and ac103 genes are newly discovered core genes in the family *Baculoviridae*. Journal of Virology 86 (22), 12069-79.

Erinnyis ello granulovirus

Ardisson-Araujo, D. M., de Melo, F. L., Andrade, M. de S., Sihler, W., Bao, S. N., Ribeiro, B. M., de Souza, M. L. (2014). Genome sequence of Erinnyis ello granulovirus (ErelGV), a natural cassava hornworm pesticide and the first sequenced shingid-infecting betabaculovirus. BMC Genomics 15, 856.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

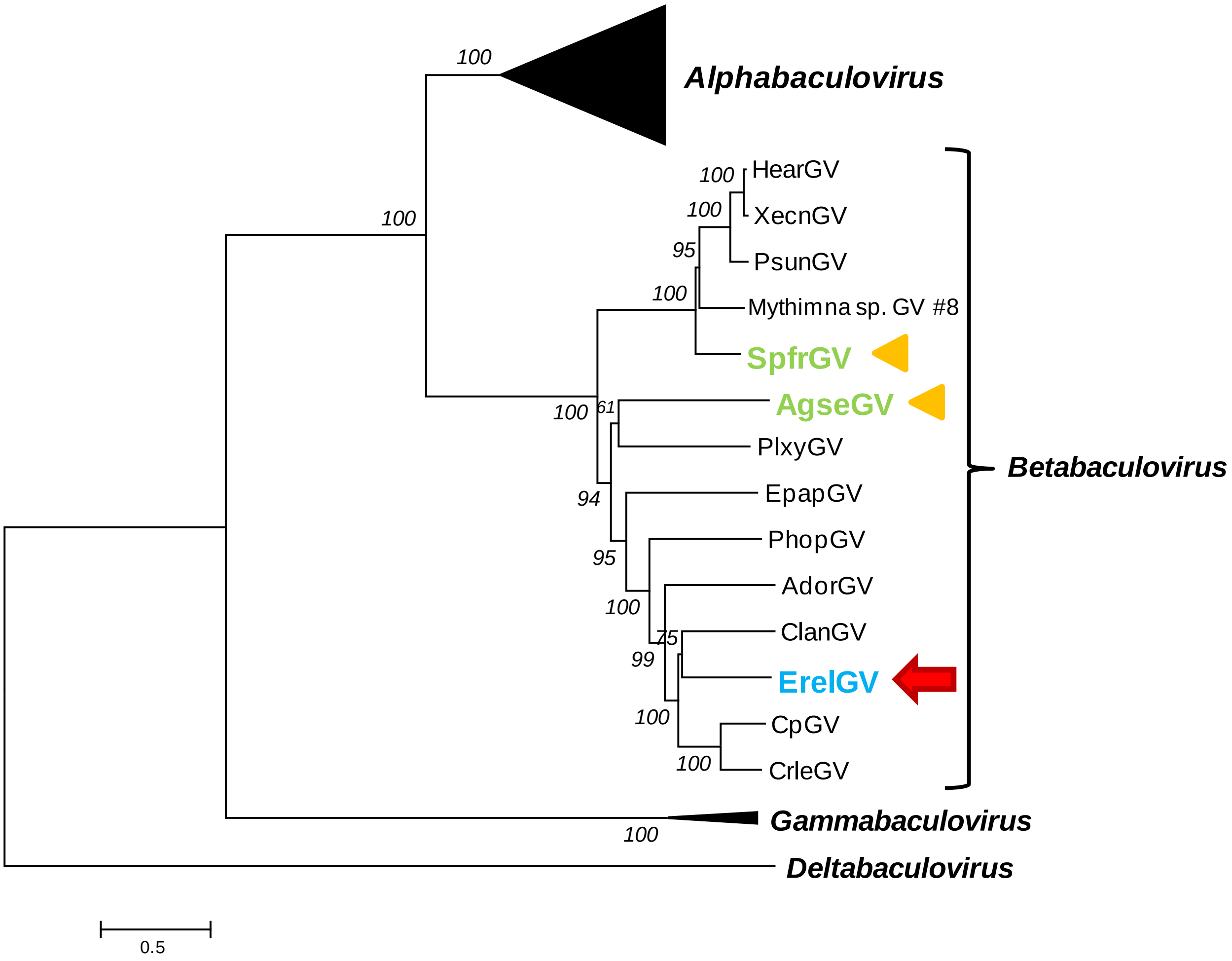

Figure 1. Relationships of baculovirus species and other isolates, inferred from the predicted amino acid sequences of baculovirus core genes. The phylogenetic tree was constructed from the concatenated alignments of 34 baculovirus core gene amino acid sequences using the minimum-evolution method using the James-Taylor-Thornton substitution model and a gamma parameter of 0.85 (estimated from the *dnapol* alignment). Bootstrap values are shown for each node. Clades corresponding to the four genera of *Baculoviridae* are indicated. The proposed species is listed in blue font and denoted with a red arrow. Additional new *Betabaculovirus* species discussed at EC47 are listed in green font and denoted with an orange arrowhead. *Betabaculovirus* taxa include the representative isolates for species *Adoxophyes orana granulovirus* (AdorGV), *Agrotis segetum granulovirus* (AgseGV), *Cryptophlebia leucotreta granulovirus* (CrleGV), *Cydia pomonella granulovirus* (CpGV), *Errinyis ello granulovirus* (ErelGV), *Helicoverpa armigera granulovirus* (HearGV), *Phthorimaea operculella granulovirus* (PhopGV), *Plutella xylostella granulovirus* (PlxyGV), *Pseudalatia unipuncta granulovirus* (PsunGV), *Spodoptera frugiperda granulovirus* (SpfrGV), *Xestia c-nigrum granulovirus* (XecnGV), as well as isolates Clostera anachoreta granulovirus (ClanGV), Epinotia aporema granulovirus (EpapGV) and Mythimna sp. granulovirus #8 (Mythimna sp. #8).

Table 1. Pairwise nucleotide distances calculated from complete *lef-8* and *lef-9* sequence alignments*

	lef-9 lef-8	1	2	3	4	5	6	7	8	9
1	AdorGV		0.453	0.435	0.417	0.486	0.409	0.461	0.486	0.486
2	CpGV	0.449		0.341	0.387	0.500	0.394	0.490	0.480	0.506
3	CrleGV	0.402	0.364		0.396	0.510	0.414	0.475	0.488	0.511
4	ErelGV	0.447	0.421	0.424		0.486	0.385	0.476	0.492	0.489
5	HearGV	0.544	0.511	0.514	0.523		0.482	0.508	0.166	0.017
6	PhopGV	0.436	0.400	0.404	0.412	0.500		0.479	0.474	0.490
7	PlxyGV	0.528	0.497	0.501	0.494	0.482	0.499		0.494	0.504
8	PsunGV	0.558	0.563	0.498	0.548	0.179	0.530	0.512		0.167
9	XecnGV	0.537	0.510	0.512	0.517	0.019	0.501	0.500	0.177	

Table 2. Pairwise nucleotide distances calculated from complete *polh* sequence alignments and *lef-8*, *lef-9*, and *polh* sequence alignments that have been concatenated together*

	Conc. polh	1	2	3	4	5	6	7	8	9
1	AdorGV		0.211	0.240	0.208	0.268	0.234	0.315	0.266	0.268
2	CypoGV	0.407		0.163	0.180	0.258	0.197	0.263	0.255	0.254
3	CrleGV	0.390	0.316		0.217	0.289	0.215	0.293	0.285	0.283
4	ErelGV	0.389	0.360	0.372		0.247	0.221	0.289	0.256	0.247
5	HearGV	0.463	0.459	0.471	0.453		0.277	0.269	0.111	0.011
6	PhopGV	0.386	0.360	0.375	0.364	0.451		0.263	0.264	0.275
7	PlxyGV	0.455	0.450	0.451	0.448	0.457	0.445		0.289	0.263
8	PsunGV	0.467	0.463	0.455	0.465	0.161	0.453	0.463		0.108
9	XecnGV	0.462	0.460	0.470	0.453	0.017	0.455	0.459	0.161	

*The numbers of base substitutions per site between pairs of sequences are shown. Abbreviations of the taxa are as listed for Figure 1. Analyses were conducted using the Kimura 2-parameter model in MEGA6. Pairwise distances for *lef-8* (Table 1) and the concatenated *lef-8*/*lef-9*/*polh* (Table 2) sequences are listed below the diagonal lines, and *lef-9* (Table 1) and *polh* (Table 2) distances are listed above the diagonal lines. Values for the proposed species are in red bold type.